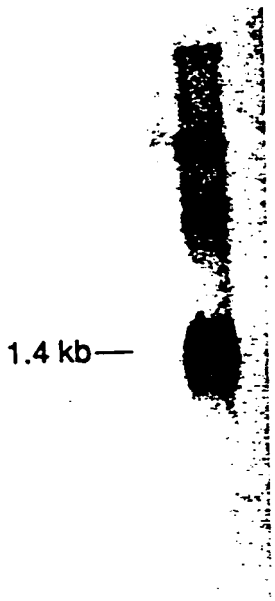

Figure 1

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121   CCAGGACCTCAAAGCACCCCCGACCTAAGGTCACCAGCCCACTGGCCCCAGACGCAGTGG    180

181   GCTCCGCTGACTCTCTTGGACACCTCCTGGGAGGAAAATGCTCCCTGTCTGCCATCGTTT    240
                                               M  L  P  V  C  H  R  F

241   TTGCGACCACCTCCTCCTCCTGCTCTTGCTGCCCTCGACGACCCTGGCCCCCGCGCCAGC    300
       C  D  H  L  L  L  L  L  L  P  S  T  T  L  A  P  A  P  A

301   ATCCATGGGCCCCGCTGCCGCCCTGCTCCAGGTTCTTGGGCTTCCCGAAGCGCCCCGGAG    360
       S  M  G  P  A  A  A  L  L  Q  V  L  G  L  P  E  A  P  R  S

361   CGTCCCCACACACCGACCTGTGCCTCCTGTCATGTGGCGCCTATTCCGTCGCCGTGACCC    420
       V  P  T  H  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P

421   CCAGGAGGCCAGAGTGGGACGCCCTCTGCGGCCATGCCACGTGGAGGAACTAGGGGTCGC    480
       Q  E  A  R  V  G  R  P  L  R  P  C  H  V  E  E  L  G  V  A

481   CGGAAACATTGTGCGCCACATCCCCGACAGCGGTCTGTCCTCCAGGCCCGCACAACCCGC    540
       G  N  I  V  R  H  I  P  D  S  G  L  S  S  R  P  A  Q  P  A

541   CAGGACCTCGGGGCTGTGCCCCGAGTGGACAGTCGTCTTTGACCTGTCGAATGTGGAGCC    600
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601   CACAGAGCGCCCAACACGCGCGCGCTTAGAGTTGCGGCTGGAGGCTGAGTGTGAAGATAC    660
       T  E  R  P  T  R  A  R  L  E  L  R  L  E  A  E  C  E  D  T

661   AGGAGGGTGGGAGCTAAGCGTGGCACTGTGGGCCGACGCAGAGCATCCAGGGCCTGAGCT    720
       G  G  W  E  L  S  V  A  L  W  A  D  A  E  H  P  G  P  E  L

721   GCTGCGCGTGCCGGCGCCACCAGGGGTGCTCCTGCGCGCAGACCTACTGGGGACTGCAGT    780
       L  R  V  P  A  P  P  G  V  L  L  R  A  D  L  L  G  T  A  V

781   AGCCGCCAACGCATCAGTGCCCTGTACTGTGCGCCTGGCGCTGTCACTGCACCCTGGGGC    840
       A  A  N  A  S  V  P  C  T  V  R  L  A  L  S  L  H  P  G  A

841   CACTGCAGCCTGTGGGCGCCTGGCTGAGGCCTCCCTGCTGCTGGTGACGCTGGACCCACG    900
       T  A  A  C  G  R  L  A  E  A  S  L  L  L  V  T  L  D  P  R

901   CCTGTGTCCCTTGCCGCGATTGCGGCGCCACACGGAGCCCAGGGTAGAAGTTGGTCCAGT    960
       L  C  P  L  P  R  L  R  R  H  T  E  P  R  V  E  V  G  P  V

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1081  AACGCTGAGGGGACCCGGCGGGCCGCCTGCACTCAACCACGCTGTGCTGCGCGCGCTCAT    1140
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1141  GCACGCAGCTGCTCCCACCCCGGGTGCAGGCTCGCCCTGCTGCGTGCCAGAGCGTCTATC    1200
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1201  ACCCATCTCCGTGCTCTTCTTCGACAATAGTGACAACGTGGTCCTGCGACACTACGAAGA    1260
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1261  CATGGTGGTGGATGAGTGTGGCTGCCGTTGACCACCCGGGACACCCTTTCAGGGACCGCC    1320
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1381  TTTGACT   1387
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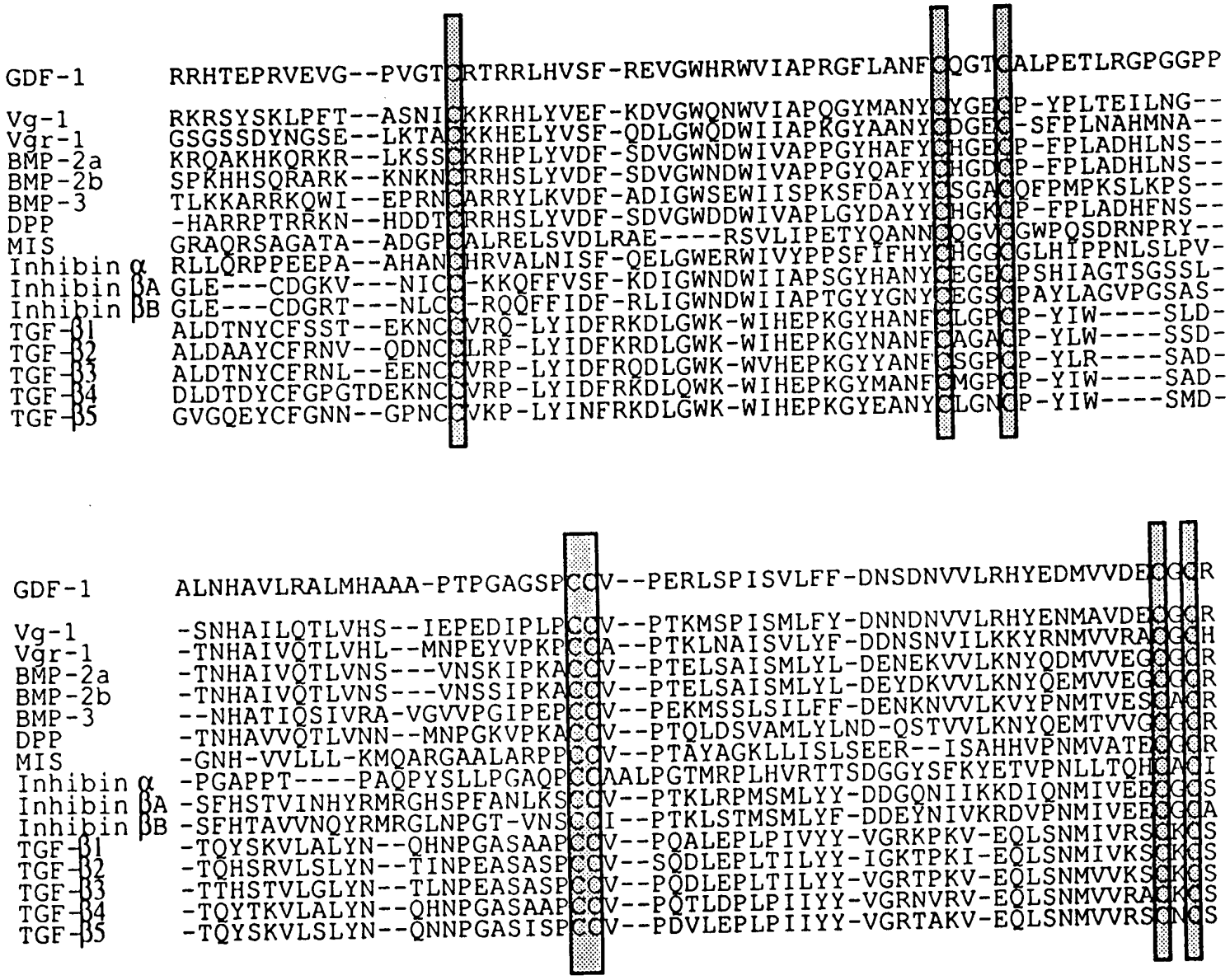
Fig. 2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BMP-2b SPKHHSQRARK--KNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCP-FPLADHLNS--
BMP-3 TLKKARRKQWI--EPRNCARRYLKVDF-ADIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS--
DPP -HARRPTRRKN--HDDTCRRHSLYVDF-SDVGWDDWIVAPLGYDAYYCHGKCP-FPLADHFNS--
MIS GRAQRSAGATA--ADGPCALRELSVDLRAE----RSVLIPETYQANNCQGVCGWPQSDRNPRY--
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Inhibin βA GLE---CDGKV---NICC-KKQFFVSF-KDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSL-
Inhibin βB GLE---CDGRT---NLCC-RQQFFIDF-RLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSAS-
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TGF-β5 GVGQEYCFGNN--GPNCCVKP-LYINFRKDLGWK-WIHEPKGYEANYCLGNCP-YIW----SMD-
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BMP-2b -TNHAIVQTLVNS---VNSSIPKACCV--PTELSAISMLYL-DEYDKVVLKNYQEMVVEGCGCR
BMP-3 --NHATIQSIVRA-VGVVPGIPEPCCV--PEKMSSLSILFF-DENKNVVLKVYPNMTVESCACR
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Inhibin βB -SFHTAVVNQYRMRGLNPGT-VNSCCI--PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEECGCA
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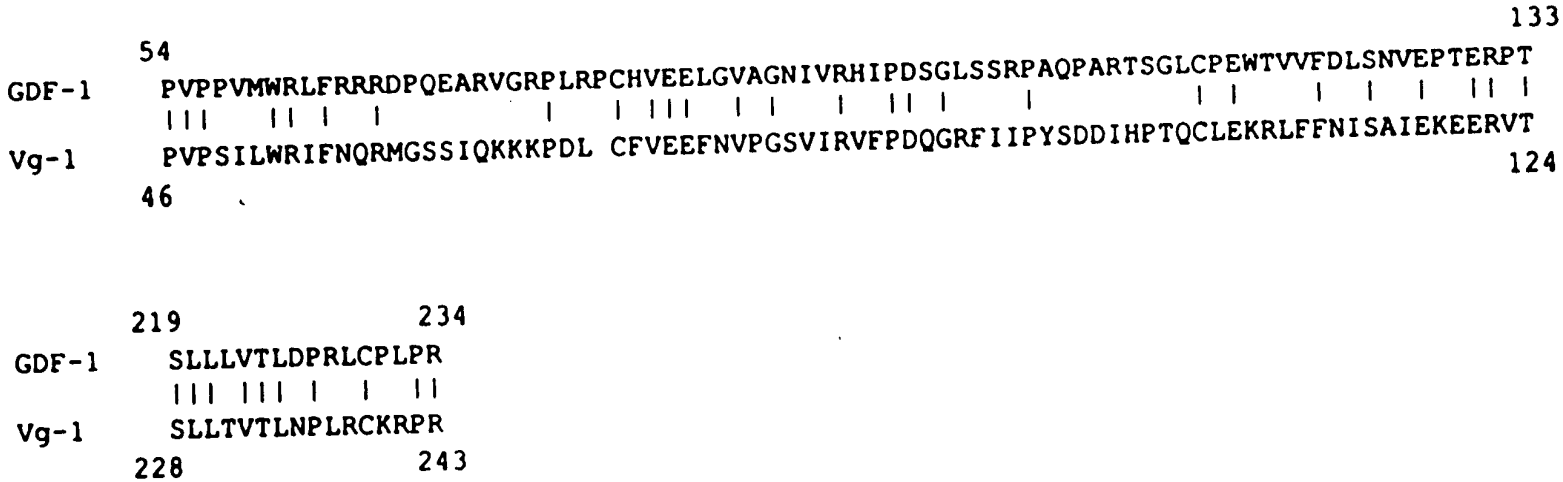
TGF-β3 -TTHSTVLGLYN--TLNPEASASPCCV--PQDLEPLTILYY-VGRTPKV-EQLSNMVVKSCKCS
TGF-β4 -TQYTKVLALYN--QHNPGASAAPCCV--PQTLDPLPIIYY-VGRNVRV-EQLSNMVVRACKCS
TGF-β5 -TQYSKVLSLYN--QNNPGASISPCCV--PDVLEPLPIIYY-VGRTAKV-EQLSNMVVRSCNCS

Figure 3a

	GDF-1	Vg-1	Vgr-1	BMP-2a	BMP-2b	BMP-3	DPP	MIS	Inhibin α	Inhibin βA	Inhibin βB	TGF-β1	TGF-β2	TGF-β3	TGF-β4	TGF-β5
GDF-1	100	52	40	38	39	41	34	33	22	31	31	26	27	30	26	26
Vg-1	–	100	59	59	57	45	49	27	23	45	40	34	35	38	33	35
Vgr-1	–	–	100	62	59	43	57	26	23	45	39	35	37	38	37	37
BMP-2a	–	–	–	100	92	44	73	26	20	42	37	34	34	35	33	33
BMP-2b	–	–	–	–	100	44	74	27	21	41	37	33	34	35	33	33
BMP-3	–	–	–	–	–	100	42	25	28	33	33	29	31	31	26	28
DPP	–	–	–	–	–	–	100	25	20	39	36	35	35	35	35	34
MIS	–	–	–	–	–	–	–	100	18	22	22	24	21	26	25	24
Inhibin α	–	–	–	–	–	–	–	–	100	23	21	24	23	24	24	24
Inhibin βA	–	–	–	–	–	–	–	–	–	100	63	38	37	36	35	38
Inhibin βB	–	–	–	–	–	–	–	–	–	–	100	35	35	36	34	32
TGF-β1	–	–	–	–	–	–	–	–	–	–	–	100	73	77	85	81
TGF-β2	–	–	–	–	–	–	–	–	–	–	–	–	100	81	68	69
TGF-β3	–	–	–	–	–	–	–	–	–	–	–	–	–	100	74	73
TGF-β4	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	78
TGF-β5	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100

Figure 3b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Vg-1 SLLTVTLNPLRCKRPR
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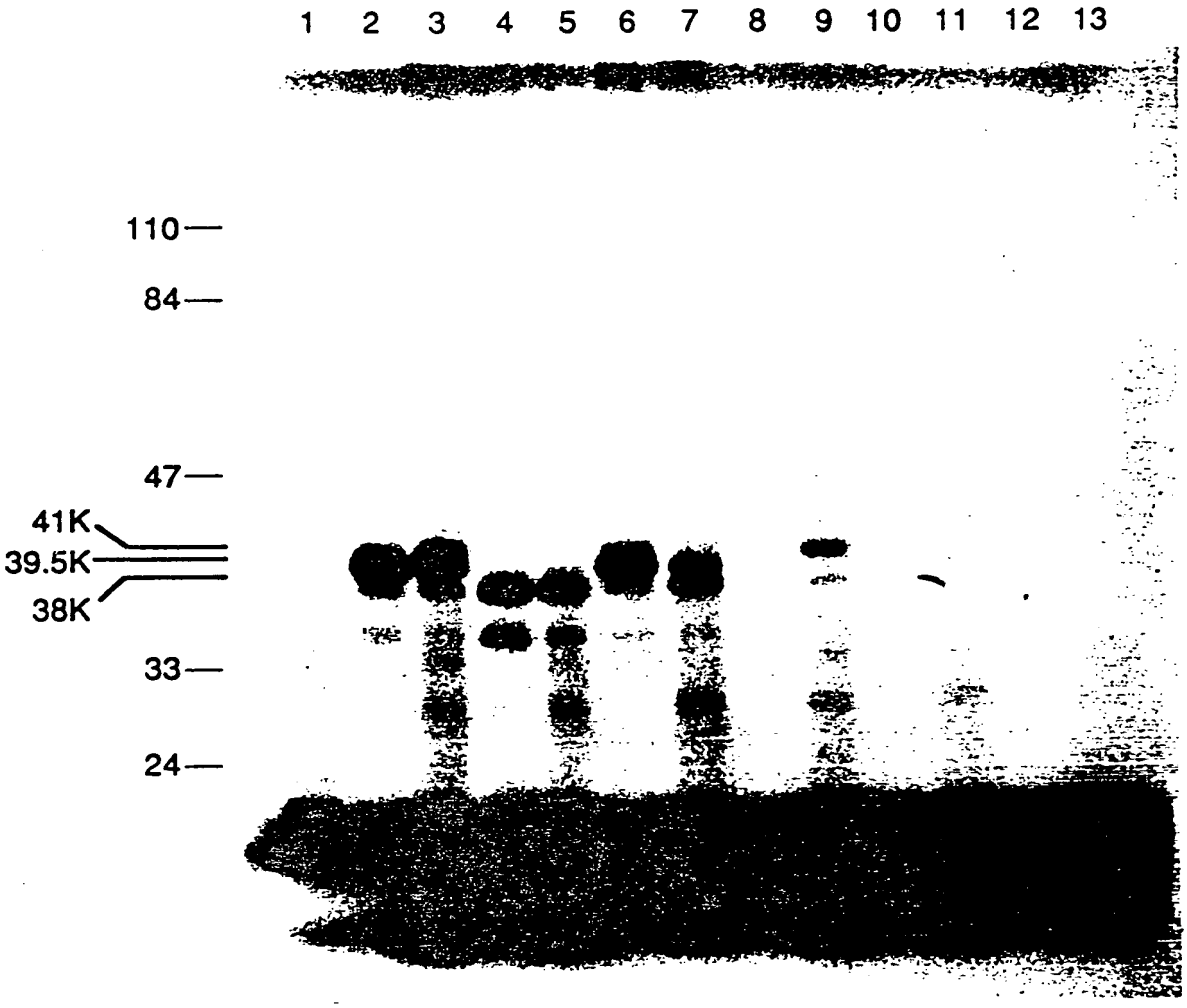
Fig 3a



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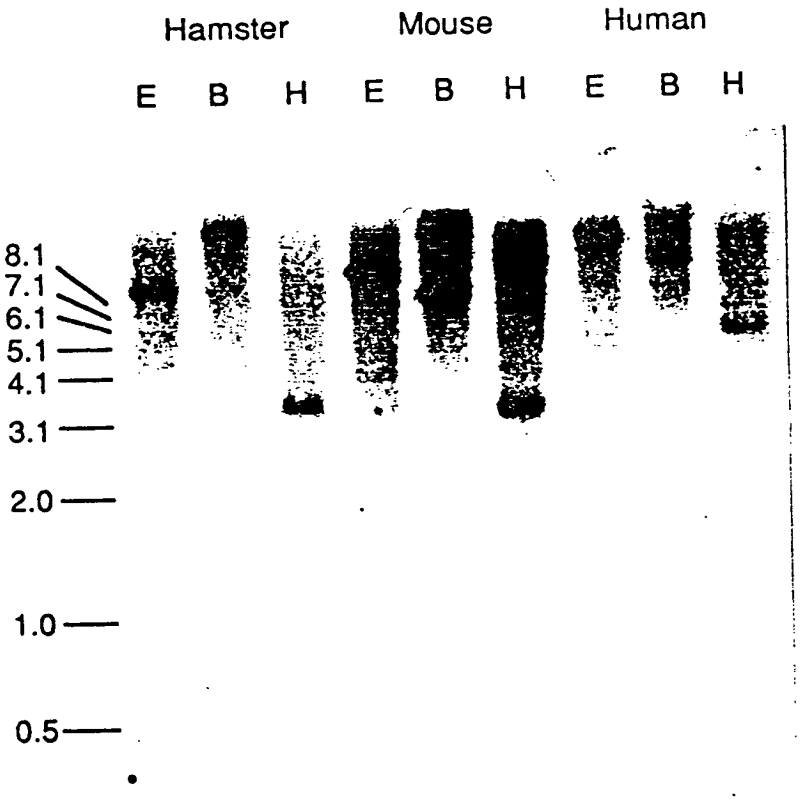

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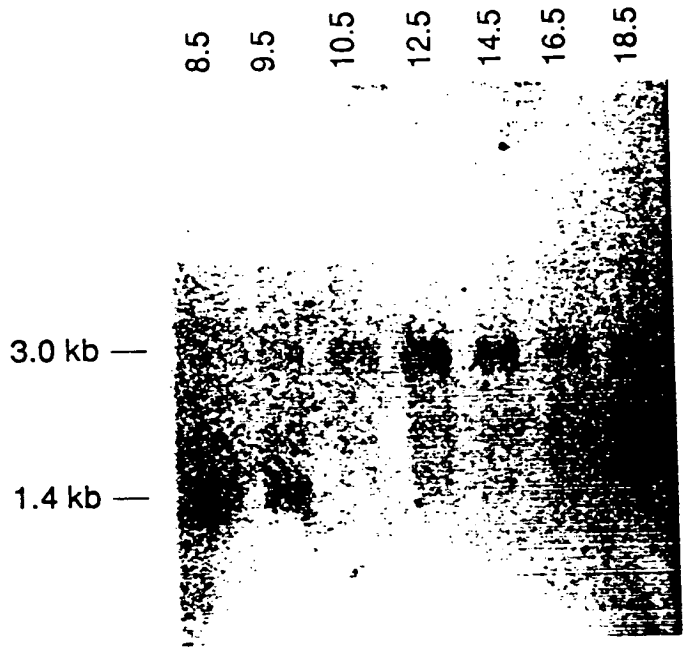

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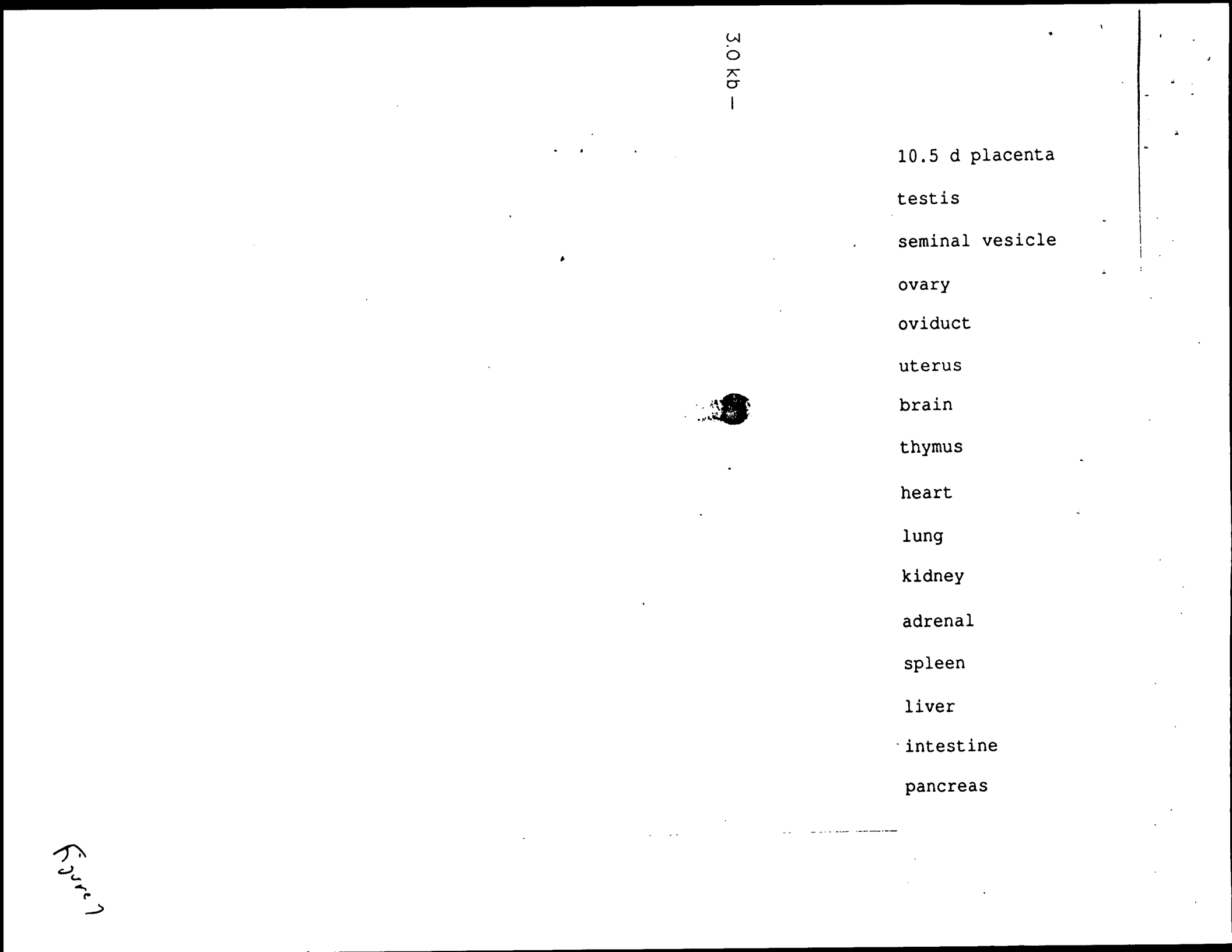
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Figure 1

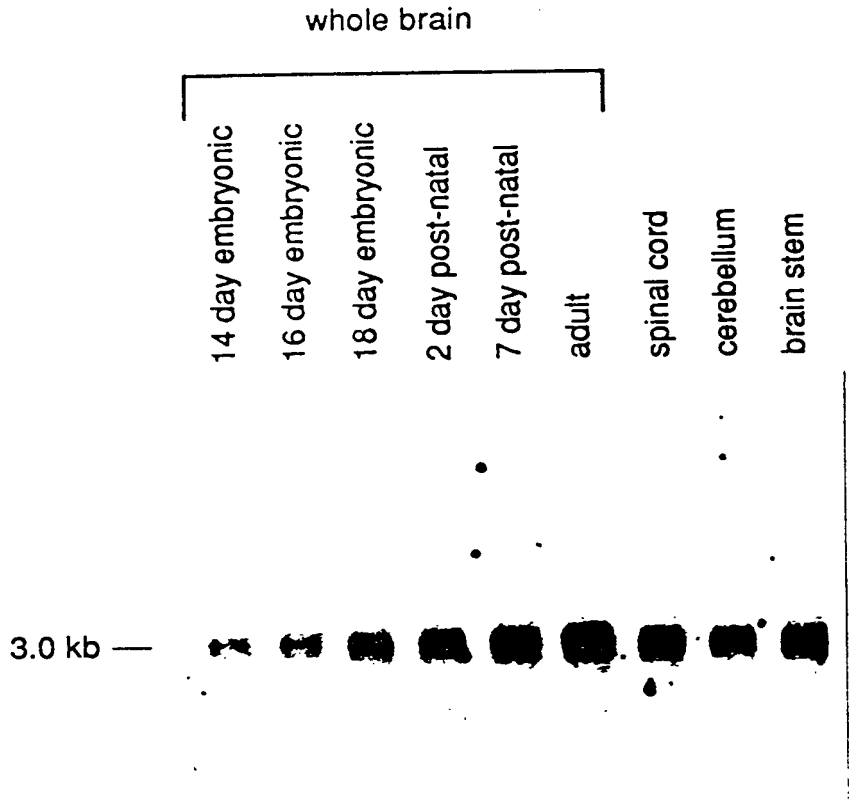
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Figure 8

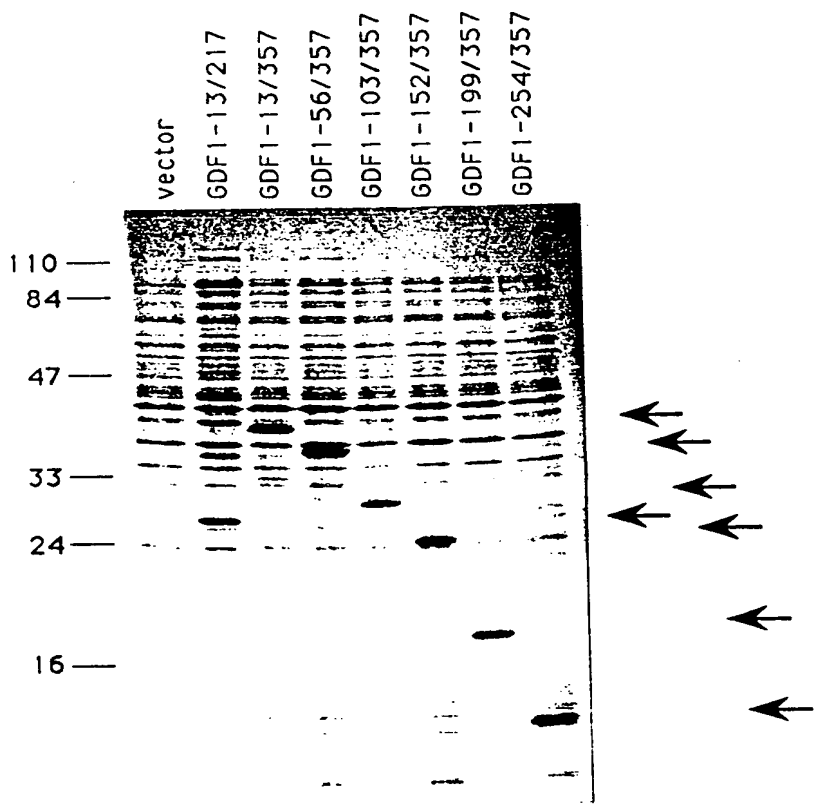
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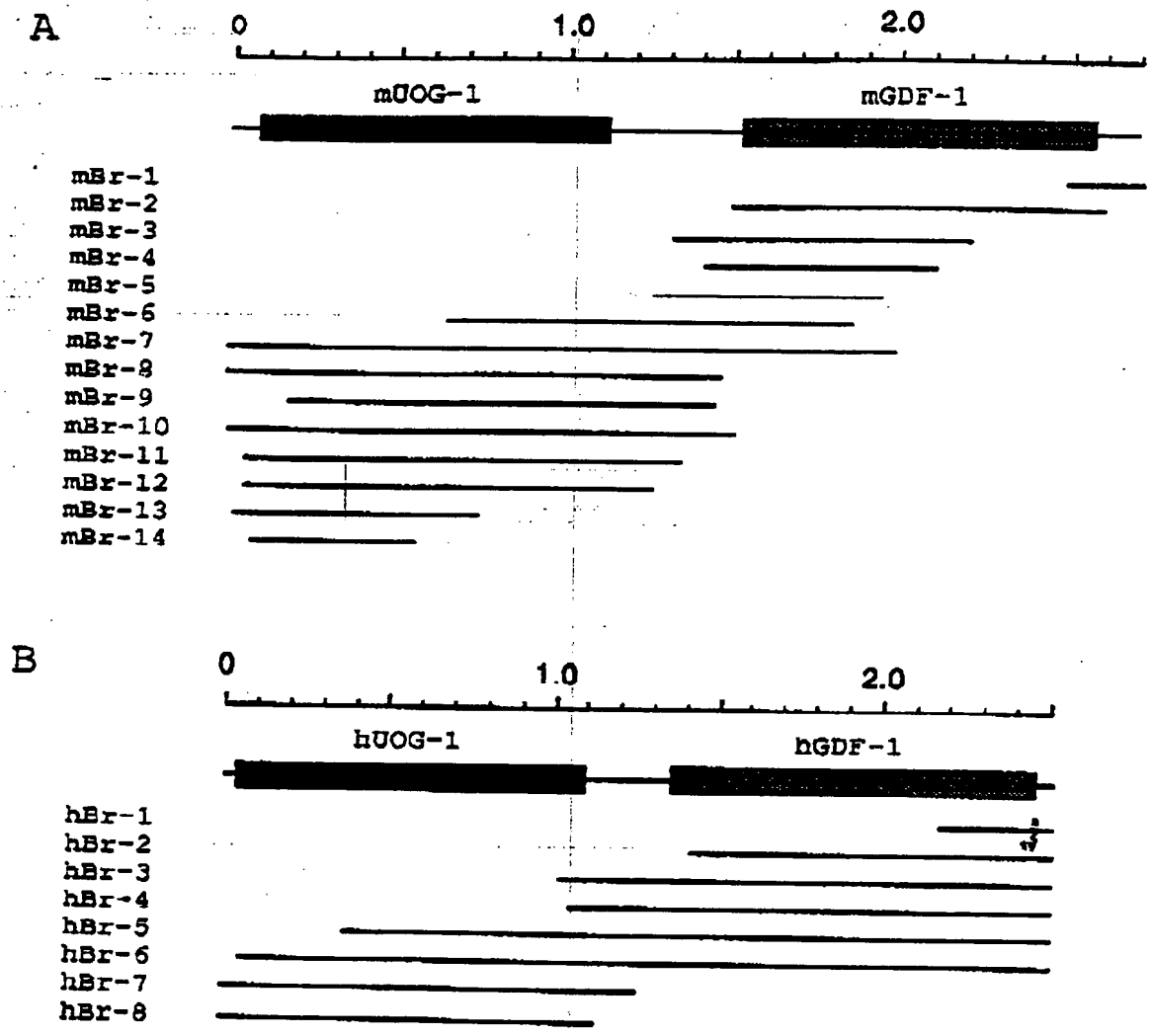
Figure 9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hBr-7
hBr-8

Figure 10

```
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2341  CCGCGTGGCTTCCTAGCCAACTTCTGCCAGGGCACGTGCGCACTACCCGAAACGCTGAGG 2400
       P  R  G  F  L  A  N  F  C  Q  G  T  C  A  L  P  E  T  L  R
2401  GGACCCGGCGGGCCGCCTGCACTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCAGCT 2460
       G  P  G  G  P  P  A  L  N  H  A  V  L  R  A  L  M  H  A  A
2461  GCTCCCACCCCGGGTGCAGGCTCGCCCTGCTGCGTGCCAGAGCGTCTATCACCCATCTCC 2520
       A  P  T  P  G  A  G  S  P  C  C  V  P  E  R  L  S  P  I  S
2521  GTGCTCTTCTTCGACAATAGTGACAACGTGGTCCTGCGACACTACGAAGACATGGTGGTG 2580
       V  L  F  F  D  N  S  D  N  V  V  L  R  H  Y  E  D  M  V  V
2581  GATGAGTGTGGCTGCCGTTGACCACCCGGGACACCCTTTCAGGGACCGCCCCACGCAAAA 2640
       D  E  C  G  C  R
2641  GCAGGGACTGTTTGTTCATGTTTTATTGGTGACAAAAAGCTTAAAACAAATTTGACTAAA 2700
2701  AATTAAGTTCC  2711
```

Fig 11A

```
1    GGACACGGCGGGCGAGCGGGCGGTATGGCGGCGGCGGGGCCCCGCGGCGGGGCCGACGGGG   60
                                M  A  A  A  A  G  P  A  A  G  P  T  G
61   CCCGAGCCCATGCCGAGCTACGCGCAGCTAGTGCAGCGCGGCTGGGGCAGCGCGCTGGCG   120
     P  E  P  M  P  S  Y  A  Q  L  V  Q  R  G  W  G  S  A  L  A
121  GCGGCGCGGGGCTGCACGGACTGCGGCTGGGGGCTGGCGCGTCGCGGCCTGGCTGAGCAC   180
     A  A  R  G  C  T  D  C  G  W  G  L  A  R  R  G  L  A  E  H
181  GCGCACCTGGCGCCGCCCGAGCTGCTGCTGCTGGCGCTCGGCGCGCTGGGCTGGACCGCG   240
     A  H  L  A  P  P  E  L  L  L  L  A  L  G  A  L  G  W  T  A
241  CTGCGCTCCGCGGCCACTGCGCGCCTCTTTCGGCCCCTGGCGAAGCGGTGCTGCCTCCAG   300
     L  R  S  A  A  T  A  R  L  F  R  P  L  A  K  R  C  C  L  Q
301  CCCAGAGATGCCGCCAAGATGCCCGAGAGCGCTTGGAAGTTTCTCTTCTACCTGGGCAGC   360
     P  R  D  A  A  K  M  P  E  S  A  W  K  F  L  F  Y  L  G  S
361  TGGAGCTACAGTGCCTACCTGCTGTTTGGCACCGACTACCCCTTCTTCCATGACCCACCA   420
     W  S  Y  S  A  Y  L  L  F  G  T  D  Y  P  F  F  H  D  P  P
421  TCTGTCTTCTACGACTGGACGCCGGGCATGGCAGTGCCACGGGACATTGCAGCCGCCTAC   480
     S  V  F  Y  D  W  T  P  G  M  A  V  P  R  D  I  A  A  A  Y
481  CTGCTCCAGGGAAGCTTCTATGGCCACTCCATCTACGCTACGCTATACATGGACACCTGG   540
     L  L  Q  G  S  F  Y  G  H  S  I  Y  A  T  L  Y  M  D  T  W
541  CGCAAGGACTCGGTGGTCATGCTGCTCCACCACGTGGTCACTCTCATCCTCATCGTCTCC   600
     R  K  D  S  V  V  M  L  L  H  H  V  V  T  L  I  L  I  V  S
601  TCCTACGCCTTCCGGTACCACAATGTGGGCATCCTTGTGCTCTTCCTGCACGATATCAGT   660
     S  Y  A  F  R  Y  H  N  V  G  I  L  V  L  F  L  H  D  I  S
661  GACGTGCAGCTTGAGTTCACCAAGCTCAACATTTACTTCAAGTCCCGCGGCGGCTCCTAC   720
     D  V  Q  L  E  F  T  K  L  N  I  Y  F  K  S  R  G  G  S  Y
721  CATCGGCTGCATGCCTTGGCAGCAGACTTGGGCTGCCTCAGCTTCGGCTTCAGCTGGTTC   780
     H  R  L  H  A  L  A  A  D  L  G  C  L  S  F  G  F  S  W  F
781  TGGTTCCGCCTCTACTGGTTCCCGCTCAAGGTCCTGTATGCCACCAGTCACTGCAGTCTG   840
     W  F  R  L  Y  W  F  P  L  K  V  L  Y  A  T  S  H  C  S  L
841  CGCACGGTGCCTGACATCCCCTTCTACTTCTTCTTCAATGCGCTCCTGCTGCTGCTCACC   900
     R  T  V  P  D  I  P  F  Y  F  F  F  N  A  L  L  L  L  L  T
901  CTTATGAACCTCTACTGGTTCCTGTACATCGTGGCGTTTGCAGCCAAGGTGTTGACAGGC   960
     L  M  N  L  Y  W  F  L  Y  I  V  A  F  A  A  K  V  L  T  G
961  CAGGTGCACGAGCTGAAGGACCTGCGGGAGTATGACACAGCCGAGGCCCAGAGCCTGAAG  1020
     Q  V  H  E  L  K  D  L  R  E  Y  D  T  A  E  A  Q  S  L  K
1021 CCCAGCAAAGCCGAGAAGCCACTGAGGAACGGCCTGGTGAAGGACAAGCGCTTCTGAACC  1080
     P  S  K  A  E  K  P  L  R  N  G  L  V  K  D  K  R  F
1081 CCTCGGCCCCGCCCCCGTGGACCCGGCCCCACCCCGAATACCCCGGCCACGCTCCCCGTC  1140
1141 CTTGGCCGCCCCTCCACCCCCTCCAACTCTGCTCCTCTAGGGCCGCCGCCACCTCCCCTG  1200
1201 GGACCCCGCCCCCTCATCCTGCCTCCATTTCCCGGCCACGCCCCCCAGGACCCCTGCCCC  1260
1261 TCCGGGGACACCGGCCCCGCCCTCAGCCCACTGGTCCCGGGCCGCCGCGGACCCTGCGCA  1320
1321 CTCTCTGGTCATCGCCTGGGAGGAAGATGCCACCGCCGCAGCAAGGTCCCTGCGGCCACC  1380
                                M  P  P  P  Q  Q  G  P  C  G  H  H
1381 ACCTCCTCCTCCTCCTGGCCCTGCTGCTGCCCTCGCTGCCCCTGACCCGCGCCCCCGTGC  1440
     L  L  L  L  A  L  L  L  P  S  L  P  L  T  R  A  P  V  P
1441 CCCCAGGCCCAGCCGCCGCCCTGCTCCAGGCTCTAGGACTGCGCGATGAGCCCCAGGGTG  1500
     P  G  P  A  A  A  A  L  L  Q  A  L  G  L  R  D  E  P  Q  G  A
1501 CCCCCAGGCTCCGGCCGGTTCCCCCGGTCATGTGGCGCCTGTTTCGACGCCGGGACCCCC  1560
     P  R  L  R  P  V  P  P  V  M  W  R  L  F  R  R  R  D  P  Q
1561 AGGAGACCAGGTCTGGCTCGCGGCGGACGTCCCCAGGGGTCACCCTGCAACCGTGCCACG  1620
     E  T  R  S  G  S  R  R  T  S  P  G  V  T  L  Q  P  C  H  V
1621 TGGAGGAGCTGGGGGTCGCCGGAAACATCGTGCGCCACATCCCGGACCGCGGTGCGCCCA  1680
     E  E  L  G  V  A  G  N  I  V  R  H  I  P  D  R  G  A  P  T
1681 CCCGGGCCTCGGAGCCTGTCTCGGCCGCGGGGCATTGCCCTGAGTGGACAGTCGTCTTCG  1740
     R  A  S  E  P  V  S  A  A  G  H  C  P  E  W  T  V  V  F  D
1741 ACCTGTCGGCTGTGGAACCCGCTGAGCGCCCGAGCCGGGCCCGCCTGGAGCTGCGTTTCG  1800
     L  S  A  V  E  P  A  E  R  P  S  R  A  R  L  E  L  R  F  A
1801 CGGCGGCGGCGGCGGCAGCCCCGGAGGGCGGCTGGGAGCTGAGCGTGGCGCAAGCGGGCC  1860
     A  A  A  A  A  A  P  E  G  G  W  E  L  S  V  A  Q  A  G  Q
1861 AGGGCGCGGGCGCGGACCCCGGGCCGGTGCTGCTCCGCCAGTTGGTGCCCGCCCTGGGGC  1920
     G  A  G  A  D  P  G  P  V  L  L  R  Q  L  V  P  A  L  G  P
1921 CGCCAGTGCGCGCGGAGCTGCTGGGCGCCGCTTGGGCTCGCAACGCCTCATGGCCGCGCA  1980
     P  V  R  A  E  L  L  G  A  A  W  A  R  N  A  S  W  P  R  S
1981 GCCTCCGCCTGGCGCTGGCGCTACGCCCCCGGGCCCCTGCCGCCTGCGCGCGCCTGGCCG  2040
     L  R  L  A  L  A  L  R  P  R  A  P  A  A  C  A  R  L  A  E
2041 AGGCCTCGCTGCTGCTGGTGACCCTCGACCCGCGCCTGTGCCACCCCCTGGCCCGGCCGC  2100
     A  S  L  L  L  V  T  L  D  P  R  L  C  H  P  L  A  R  P  R
2101 GGCGCGACGCCGAACCCGTGTTGGGCGGCGGCCCCGGGGGCGCTTGTCGCGCGCGGCGGC  2160
     R  D  A  E  P  V  L  G  G  G  P  G  G  A  C  R  A  R  R  L
2161 TGTACGTGAGCTTCCGCGAGGTGGGCTGGCACCGCTGGGTCATCGCGCCGCGCGGCTTCC  2220
     Y  V  S  F  R  E  V  G  W  H  R  W  V  I  A  P  R  G  F  L
2221 TGGCCAACTACTGCCAGGGTCAGTGCGCGCTGCCCGTCGCGCTGTCGGGGTCCGGGGGGC  2280
     A  N  Y  C  Q  G  Q  C  A  L  P  V  A  L  S  G  S  G  G  P
2281 CGCCGGCGCTCAACCACGCTGTGCTGCGCGCGCTCATGCACGCGGCCGCCCCGGGAGCCG  2340
     P  A  L  N  H  A  V  L  R  A  L  M  H  A  A  A  A  P  G  A  A
2341 CCGACCTGCCCTGCTGCGTGCCCGCGCGCCTGTCGCCCATCTCCGTGCTCTTCTTTGACA  2400
     D  L  P  C  C  V  P  A  R  L  S  P  I  S  V  L  F  F  D  N
2401 ACAGCGACAACGTGGTGCTGCGGCAGTATGAGGACATGGTGGTGGACGAGTGCGGCTGCC  2460
     S  D  N  V  V  L  R  Q  Y  E  D  M  V  V  D  E  C  G  C  R
2461 GCTAACCCGGGGCGGGCAGGGACGCGGGCCCAACAATAAATGCCGCGTGG  2510
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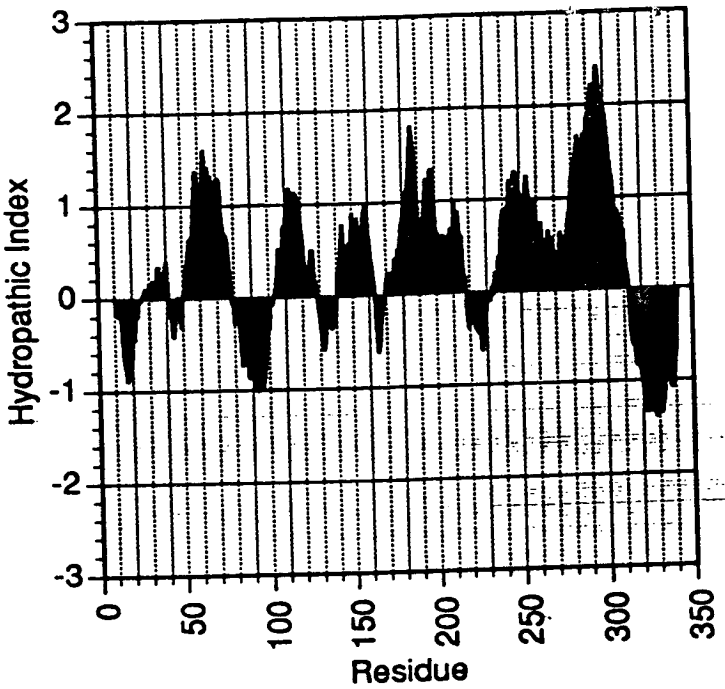
Fig 11B


Hydropathic Index
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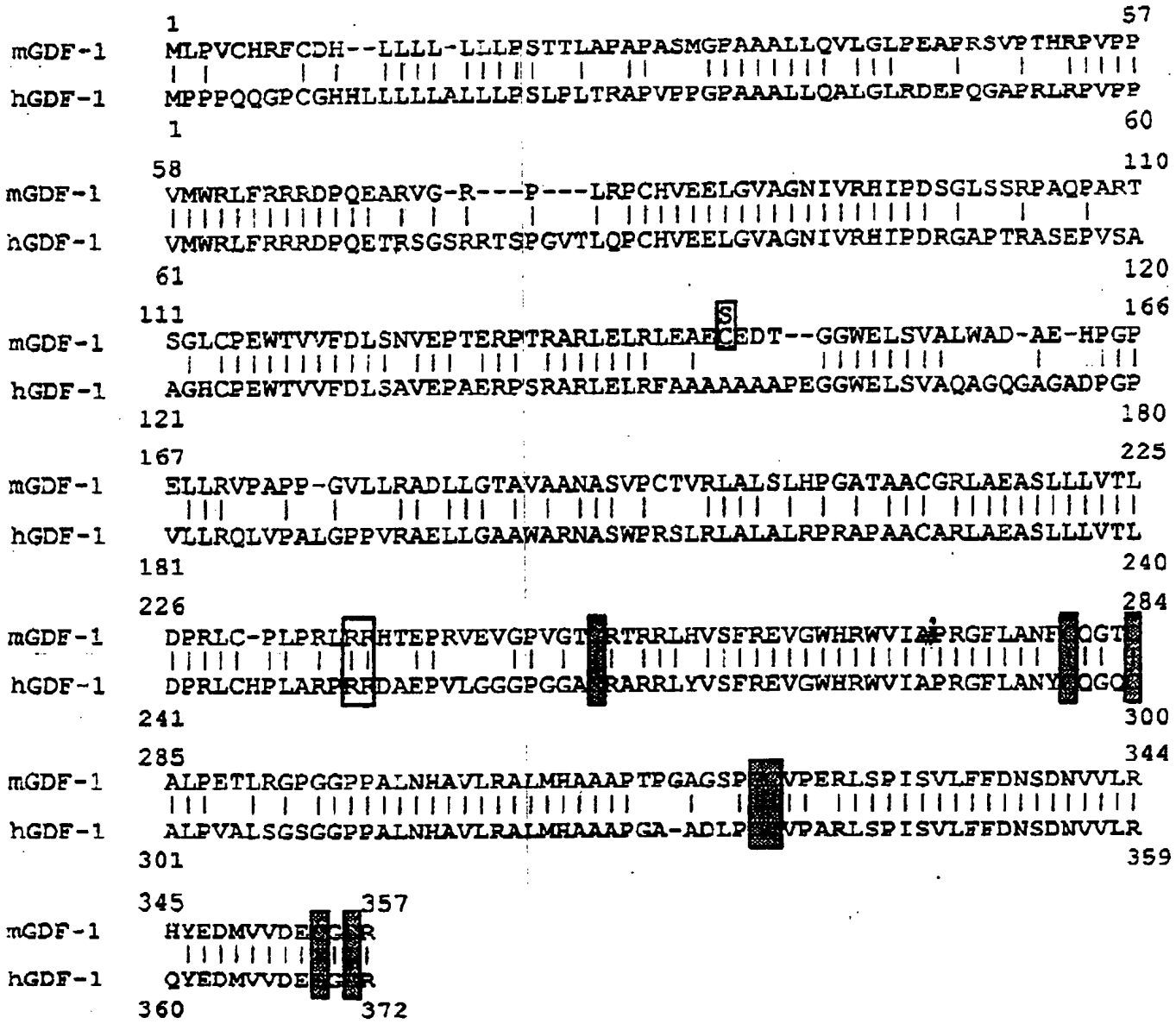
2
1
0
-1
-2
-3
0
50
100
150
200
250
300
350
Residue

Fig 12


1 57
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hGDF-1 MPPPQQGPCGHHLLLLLALLLPSLPLTRAPVPPGPAAALLQALGLRDEPQGAPRLRPVPP
1 60
58 110
mGDF-1 VMWRLFRRRDPQEARVG-R---P---LRPCHVEELGVAGNIVRHIPDSGLSSRPAQPART
hGDF-1 VMWRLFRRRDPQETRSGSRRTSPGVTLQPCHVEELGVAGNIVRHIPDRGAPTRASEPVSA
61 120
111 166
mGDF-1 SGLCPEWTVVFDLSNVEPTERPTRARLELRLEAPCEDT--GGWELSVALWAD-AE-HPGP
hGDF-1 AGHCPEWTVVFDLSAVEPAERPSRARLELRFAAAAAAAPEGGWELSVAQAGQGAGADPGP
121 180
167 225
mGDF-1 ELLRVPAPP-GVLLRADLLGTAVAANASVPCTVRLALSLHPGATAACGRLAEASLLLVTL
hGDF-1 VLLRQLVPALGPPVRAELLGAAWARNASWPRSLRLALALRPRAPAACARLAEASLLLVTL
181 240
226 284
mGDF-1 DPRLC-PLPRLRRHTEPRVEVGPVGTARTRRLHVSFREVGWHRWVIAPRGFLANFSQGT
hGDF-1 DPRLCHPLARPRRDAEPVLGGGPGGACRARRLYVSFREVGWHRWVIAPRGFLANYAQGQ
241 300
285 344
mGDF-1 ALPETLRGPGGPPALNHAVLRALMHAAAPTPGAGSPCVPERLSPISVLFFDNSDNVVLR
hGDF-1 ALPVALSGSGGPPALNHAVLRALMHAAAPGA-ADLPCVPARLSPISVLFFDNSDNVVLR
301 359
345 357
mGDF-1 HYEDMVVDECGCR
hGDF-1 QYEDMVVDECGCR
360 372

Fig 8a

```
                1                                                          60
mUOG-1          MAAAAATPRLEAPEPMPSYAQMLQRSWASALAAAQGCGDCGWGLARRGLAEHAHLAAPEL
                |||| |||||||||  || | ||||||  || ||||||||||||||||||| |||
hUOG-1          MAAAGPAAGPTGPEPMPSYAQLVQRGWGSALAAARGCTDCGWGLARRGLAEHAHLAPPEL
                1                                                          60

               61                                                         120
mUOG-1          LLAVLCALGWTALRWAATTHIFRPLAKRCRLQPRDAARLPESAWKLLFYLACWSYCAYLL
                ||  | |||||||| |||   |||||||| ||||||| ||||||  ||||  ||| ||||
hUOG-1          LLLALGALGWTALRSAATARLFRPLAKRCCLQPRDAAKMPESAWKFLFYLGSWSYSAYLL
               61                                                         120

              121                                                         180
mUOG-1          LGTSYPFFHDPPSVFYDWRSGMAVPWDIAVAYLLQGSFYCHSIYATVYMDSWRKDSVVML
                 || |||||||||||||||  |||||  ||| |||||||||  |||||||  ||| ||||||||||
hUOG-1          FGTDYPFFHDPPSVFYDWTPGMAVPRDIAAAYLLQGSFYGHSIYATLYMDTWRKDSVVML
              121                                                         180

              181                                                         240
mUOG-1          VHHVVTLLLIASSYAFRYHNVGLLVFFLHDVSDVQLEFTKLNIYFKARGGAYHRLHGLVA
                ||||||  ||  |||||||||||  ||  ||||  |||||||||||||||||  |||  |||||  | |
hUOG-1          LHHVVTLILIVSSYAFRYHNVGILVLFLHDISDVQLEFTKLNIYFKSRGGSYHRLHALAA
              181                                                         240

              241                                                         300
mUOG-1          NLGCLSFCFCWFWFRLYWFPLKVLYATCHCSLQSVPDIPYYFFFNILLLLLLMVMNIYWFL
                ||||||  |  ||||||||||||||||||  ||||  |||||  |||||  |||||  |||||||
hUOG-1          DLGCLSFGFSWFWFRLYWFPLKVLYATSHCSLRTVPDIPFYFFFNALLLLLTLMNLYWFL
              241                                                         300

              301                                                         350
mUOG-1          YIVAFAAKVLTGQMRELEDLREYDTLEAQTAKPCKAEKPLRNGLVKDKLF
                ||||||||||||  ||  |||||||  |||  ||  ||||||||||||||  |
hUOG-1          YIVAFAAKVLTGQVHELKDLREYDTAEAQSLKPSKAEKPLRNGLVKDKRF
              301                                                         350
```

Fig 13b

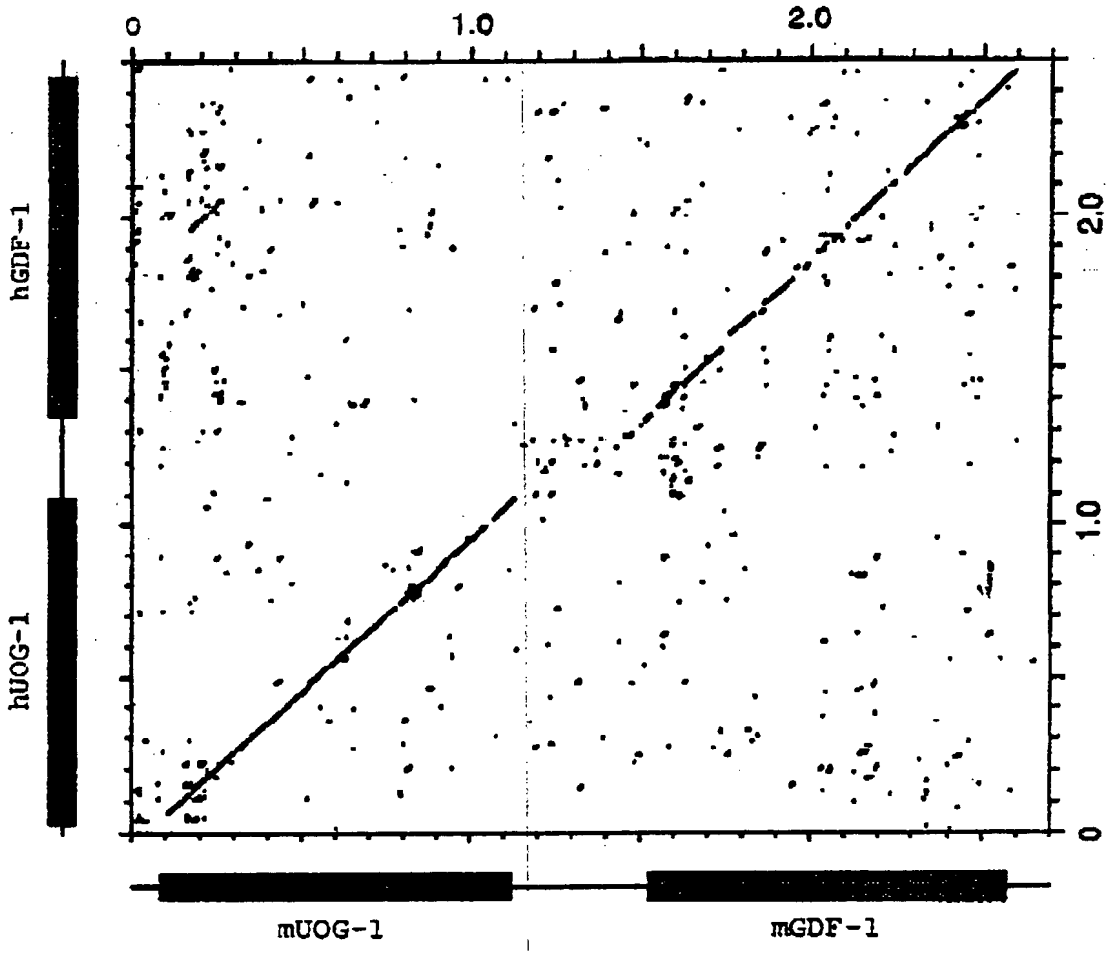
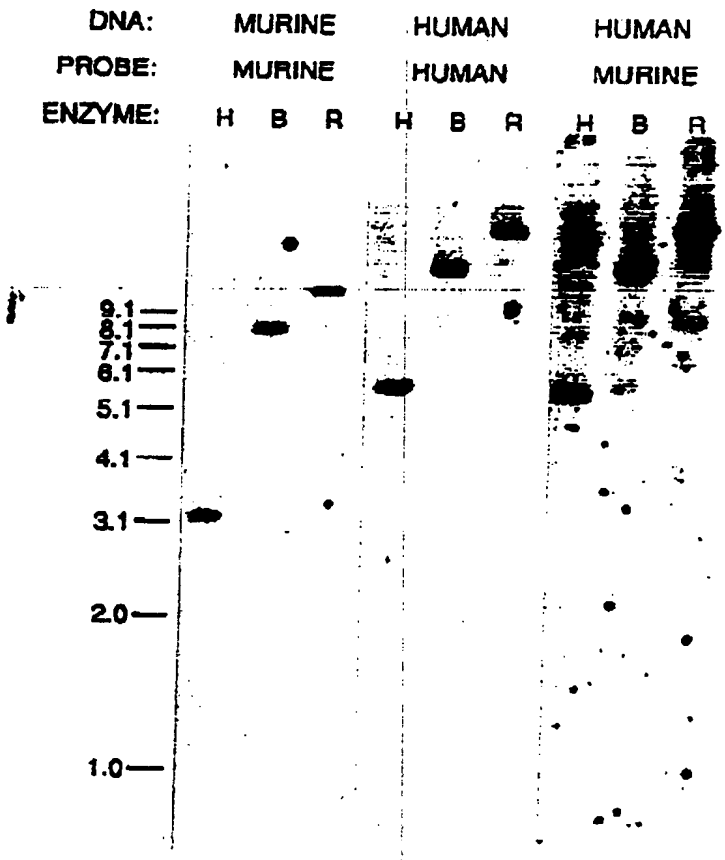


Fig 13c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HUMAN
HUMAN
PROBE:
MURINE
HUMAN
MURINE
ENZYME:
H B R H B R H B R
9.1
8.1
7.1
6.1
5.1
4.1
3.1
2.0
1.0

Fig 14